

DE 01-OCT-2003 (TREMBLrel. 25; Last annotation update)

DE Putative matrix cell adhesion molecule-3.

OS Homo sapiens (Human).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID:9606;

RN 11] SEQUENCE FROM N.A.

RA Telson M. D ;

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ database.

DR EMBL; AY039025; AAKB2649.1; -;

DR HSSP; P01869; IAB6.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR00596; Ig_v.

DR SMART; SM00406; IgV; 1.

DR PROSITE; PS50835; Ig_LIKE; 1.

DR SEQUENCE; 159 AA; 1749 MW; 5D29537E881FAF02 CRC64;

Query Match 65.5%; Score 390.5; DB 2; Length 159;

Best Local Similarity 60.0%; Pred. No. 3.1e-33; Matches 78; Conservative 16; Mismatches 19; Indels 17; Gaps 2;

DE 80 AOKFQGVMTMDTSTVYMLSSLRSLSEDVAVYC 115

Qy 1 VOLLEOSGAEVKPGASVTISQASRDPFGQYIHWYRQAPQGFEWNGINPSSGGSANY 60

Db 21 VOLV-QSGAEVVKPGASVVKVSCKASGFTFSNVYMWQRQAPQGFEWNGINPSSGGSARY 79

Qy 61 APKFKGKLTMSDSDSTVYMLTSLEDTAVYCYCILQ-----ALKHW 104

Db 80 SOKFQGVMTMDTSTVYMLSSLRSLSDTAVYFCAREMEITFGAVSKGFYYGMDVW 139

Qy 105 CGTGLAVSS 114

Db 140 GQGTTVTVSS 149

RESULT 3

HV1B_HUMAN STANDARD; PRT; 117 AA.

ID P01743; 2017-03-21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V-I region HG3 precursor.

OS Homo Sapiens (Human).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID:9606;

RN 11] SEQUENCE FROM N.A.

RP MEDLINE=83144028; PubMed=6298778;

RA Rechavi G., Ram D., Glazer L., Zakkut R., Givoli D.; Rechavi G., Ram D., Glazer L., Zakkut R., Givoli D.;

RT "Evolutionary aspects of immunoglobulin heavy chain variable region (VH) gene subgroups." ; U.S.A. 80:855-859(1983).

RT Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).

RL 1- SIMILARITY: Contains 1 immunoglobulin-like domain.

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CC EMBL; J00240; AIA5298.1; -;

CC PIR; A02024; HXRORG.

DR HSSP; P01751; IINQB.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:003823; F:antigen binding; NAS.

DR GO; GO:000955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.

DE 09N095 PRELIMINARY; PRT; 475 AA.

DR SMART; SM00406; IgV; 1.

DR PROSITE; PS50835; Ig_LIKE; 1.

DR Immunglobulin V region; Signal.

DR SIGNAL 1 19

FT CHAIN 20 117 Ig heavy chain V-I region HG3.

FT DOMAIN 20 >117 Ig-like.

FT NON_TER 117 117

DE 63.2%; Score 376.5; DB 1; Length 117;

Best Local Similarity 74.0%; Pred. No. 6.6e-32; Matches 71; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

DE 80 AOKFQGVMTMDTSTVYMLSSLRSLSEDVAVYC 115

Qy 1 VOLLEOSGAEVKPGASVTISQASRDPFGQYIHWYRQAPQGFEWNGINPSSGGSANY 60

Db 21 VOLV-QSGAEVVKPGASVVKVSCKASGFTFSNVYMWQRQAPQGFEWNGINPSSGGSARY 79

Qy 61 APKFKGKLTMSDSDSTVYMLTSLEDTAVYCYCILQ-----ALKHW 104

Db 80 SOKFQGVMTMDTSTVYMLSSLRSLSDTAVYFCAREMEITFGAVSKGFYYGMDVW 139

DE (Fragment).

OS Homo Sapiens (Human).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID:9606;

RN 11] SEQUENCE FROM N.A.

RP MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal Clin. Immunopathol. 87:184-192(1998)."

DR EMBL; AF035019; AAD56255.1; -;

DR HSSP; P01751; IINQB.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR SMART; SM00406; IgV; 1.

DR PROSITE; PS50835; Ig_LIKE; 1.

FT NON_TER 125 125

FT NON_TER 125 AA; 13516 MW; 0D3CD5C23488EAC CRC64;

Qy 1 VOLLEOSGAEVKPGASVTISQASRDPFGQYIHWYRQAPQGFEWNGINPSSGGSANY 60

Db 2 VOLVE-SGAEVVKPGASVVKVSCKASGFTFSNVYMWQRQAPQGFEWNGINPSSGGSARY 60

Qy 61 APKFKGKLTMSDSDSTVYMLTSLEDTAVYCYCILQ-----QALKHWGQOCL 109

Db 61 AOKFQGVMTMDTSTVYMLSSLRSLSDTAVYFCAREMEITFGAVSKGFYYGMDVW 120

Qy 110 VAVSS 114

Db 121 VTVSS 125

RESULT 5

DE 09N095 PRELIMINARY; PRT; 475 AA.

RESULT 8			AC 0652CB;
HV1C_HUMAN			DT 25-OCT-2004 (TRIMBLrel. 28, Created)
ID HV1C_HUMAN	STANDARD;	PRT;	DT 25-OCT-2004 (TRIMBLrel. 28, Last sequence update)
AC P01744;			DT 25-OCT-2004 (TRIMBLrel. 28, Last annotation update)
DT 21-JUL-1986 (Rel. 01, Created)			DB Single-chain Fv (Fragment).
DT 16-OCT-2001 (Rel. 40, Last sequence update)			GN Name=sFv;
DT 05-JUL-2004 (Rel. 44, Last annotation update)			OS Homo Sapiens (Human).
DE Ig heavy chain V-I region ND precursor (Fragments).			OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OS Homo sapiens (Human).			OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			OX NCBI_TaxID=9606;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			RN [1]
OX NCBI_TaxID=9606;			RP SQQUENCE FROM N.A.
RN [1]			RA MEDLINE=97562799; PubMed=9219263;
RP SEQUENCE FROM N.A.			RL Kontemann R.E., Wing M.G., Winter G.;
RX MEDLINE=83005234; PubMed=6815656;			RT "Complement recruitment using bispecific diabodies."
RA Bell L.O., Gould H.J.,			DR Nat. Biotechnol. 15:629-631(1997).
RT "Cloning and sequence determination of the gene for the human			DR EMBL; Y13057; CMA7300.1; -.
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";			DR InterPro; IPR00599; Ig
Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).			DR InterPro; IPR01110; Ig-like.
RN [2]			DR InterPro; IPR00596; Ig_v.
RP SEQUENCE OF 20-147.			DR Pfam; PF00047; Ig; 2.
RA Bernich H.H., Johannsson S.G.O., von Bahr-Lindstrom H.;			DR SMART; SM00409; Ig; 2.
RL Bach M.K. (Eds.);			DR SMART; SM00406; Ig_v; 2.
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,			DR PROSITE; PS50815; Ig_LIKE; 2.
CC -1- MISCCELLANEOUS: This epsilon chain was isolated from a myeloma			FT NON_TER 1
CC protein.			FT NON_TER 1
CC -- SIMILARITY: Contains 1 immunoglobulin-like domain.			FT 244 AA; 244
DR HSPB; P01751; INQB.			FT 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;
DR GO; GO:0005576; C:extracellular; NAS.			SO SEQUENCE
DR GO; GO:0010323; F:antigen binding; NAS.			Query Match
DR GO; GO:0006955; P:immune response; NAS.			Best Local Similarity
DR InterPro; IPR007110; Ig-like.			59.1%; Score 352; DB 2; Length 244;
DR InterPro; IPR003596; Ig_v.			Matches 68; Conservative 56.2%; Pred. No. 66-29; Length 244;
DR SMART; SM00406; Ig_v; 1.			DB 18; Mismatches 27; Indels 8; Gaps 2;
DR PROSITE; PS50835; Ig_LIKE; 1.			QY 1 VOLLEQSGAEVKGPGASVTISQASRQDPFSGQYIHWYRQARQGQFENGIINPGSGSANY 60
KW direct protein sequencing; Immunoglobulin V region;			2 VOLV-QSGAEVKGPGDSVKVSQKASGVTFSQDHYMHWRQAPQGQGLEKNGWIDPNNGDTRF 60
KW Pyrrolidone carboxylic acid; Signal.			61 AKPKFGQIUMSDSSTDVYMLTSU7SED7AVYVYC-----LQLQALKHNGQGTIVAVS 113
FT SIGNAL 1			61 AORFGQRTMRTDTSIAYMVEVSRLSDTAVVYCAREGTSAIYGMDDVNGQGTIVVS 120
FT CHAIN 20	147	Ig heavy chain V-I region ND.	QY 114 S 114
FT DOMAIN 20	131	Ig-like.	Db 121 S 121
FT MOD_RES 20	20	Pyrrolidone carboxylic acid.	
FT DISULFID 41	115		
FT CONFLICT 21	21	T -> V (in Ref. 2).	
FT CONFLICT 53	54	TH -> HT (in Ref. 2).	
FT CONFLICT 67	68	VG -> GV (in Ref. 2).	
FT CONFLICT 125	125	Missing (in Ref. 2).	
FT NON_TER 147	147		
SO SEQUENCE 147 AA; 1649 MW; 94F9F72A5366C20 CRC64;			
Query Match 59.7%; Score 356; DB 1; Length 147;			
Best Local Similarity 54.4%; Pred. No. 1-3e-29;			
Matches 68; Conservative 15; Mismatches 28; Indels 14; Gaps 1;			
QY 4 LEOSGAEVKGPGASVTISQASRQDPFSGQYIHWYRQARQGQFENGIINPGSGSANY 63			
Db 23 LVSGAEVKGPGASVTISQASRQDPFSGQYIHWYRQARQGQFENGIINPGSGTNPYPR 82			
Query Match 59.7%; Score 356; DB 1; Length 147;			
Best Local Similarity 54.4%; Pred. No. 1-3e-29;			
Matches 68; Conservative 15; Mismatches 28; Indels 14; Gaps 1;			
QY 64 PFKRGLTMSRDSSTDVYMLTSU7SED7AVYVYC-----ALKHWGQTL 109			
Db 83 FQGRGTMTRDASFTAYMDLRSLSRDSAVFCAKSDPEWSDVNFDSYTLDWGQGTT 142			
QY 110 VAVSS 114			
Db 143 VTVSS 147			
RESULT 9			
Q652C8 ID Q652C8	PRELIMINARY;	PRT;	244 AA.


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Db          64 FRSKATLTVDKSSTAVMQQLSITSDSAVYCARRGWEANDYWGCGTSVTVSS 117
RESULT 14
O9UL89          PRELIMINARY;          PRT;          116 AA.
ID          O9UL89
AC          O9UL89;
DT          01-MAY-2000 (TREMBLrel. 13, Created)
DT          01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT          01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE          Myosin-reactive immunoglobulin heavy chain variable region
DE          (fragment).
OS          Homo sapiens (Human).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Primates; Cetartiodactyla; Hominoidea; Homo.
OC          NCBI_TAXID=9606;
RN          [1] SEQUENCE FROM N.A.
RP          SEQUENCE FROM N.A.
RX          MEDLINE=98277139; PubMed=9614934; DOI=10.1005/clin.1998.4531;
RA          Wu X.; Liu B.; Van der Meeve P.L.; Kalis N.N.; Berney S.M.; Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus"; Clin. Immunol. Immunopathol. 87:184-192(1998).
RL          Immuno. Immunopathol. 87:184-192(1998).
DR          EMBL; AF035025; AAD62611; -;
DR          PIR; PH0870; PH0870;
DR          PIR; PH1671; PH1671;
DR          HSSP; P01751; INMB;
DR          InterPro; IPR07110; Ig-like.
DR          InterPro; IPR03596; Ig_V.
DR          SMART; SM00406; IgV; 1.
DR          PROSITE; PS50815; Ig_LIKE; 1.
FT          1
FT          NON_TER 1
FT          1
SQ          SEQUENCE          116 AA;          12605 MW;          C8FP131DE13EA898 CRC64;
Query          Match          57.0%;          Score 340;          DB 2;          Length 116;
Best          Local Similarity          60.9%;          PRT;          117 AA.
Matches          70;          Conservative 10;          Mismatches 29;          Index 6;          Gaps 1;
Ov          6 OSGAEVKRPAGASVITIQCASRODPFSGOYIHWNRQAPQGQFENNGININPSSGSANVAPKFK 65
Db          2 OSGAEVKRPAGASVITIQCASRODPFSGOYIHWNRQAPQGQFENNGININPSSGSANVAPKFK 65
Ov          66 GRLTMSRSSTOTVWMLTSLOSDPDTAVYCYLQ----ALKHKGQGTIVAVSS 114
Db          62 GRVTITADKSTSTAVMELSLRSQEDTAVYCYASSNNGPYWFDLWGRGTLTVSS 116

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RESULT 15

HV1G_HUMAN	HV1G_HUMAN	STANDARD	PRT	117 AA.
AC P23083;	DT 01-NOV-1991 (Rel. 20, Created)	DT 01-NOV-2003 (Rel. 42, Last annotation update)	DT 10-DEC-2003 (Rel. 42, Last annotation update)	
OS Homo sapiens (Human).	OC Mammalia; Eutheria; Primates; Cetartiodactyla; Vertebrata; Euteleostomi; OX NCBI_TAXID=9606;	NCBI_TAXID=9606;		
RN [1] SEQUENCE FROM N.A.	RP MEDLINE=88295408; PubMed=2841108;	RA Matsuda F., Lee H.H., Nakai S., Sato T., Kodaira M., Zong S.Q., Ohno H.; Fukuhara S., Honjo T.; "Dispersed localization of D segments in the human immunoglobulin heavy-chain locus"; EMBO J. 7:1047-1051(1988).	RT 1-1 SIMILARITY: Contains 1 immunoglobulin-like domain.	
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GenCore version 5.1.6
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OM protein - protein search, using 8W model

Run on: November 9, 2005, 05:52:18 ; Search time 39 Seconds
 (without alignments)
 281.249 Million cell updates/sec

Title: US-09-936-964a-36
 Perfect score: 596

Sequence: 1 VOLLEQSGAEVKGPGASVTLVAVSS 114

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : PIR 79.4
 1: pir1:
 2: pir2:
 3: pir3:
 4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Best Local Similarity

81; Conservative

Mismatches

15; Indels

14; Gaps

2; Matches

53.8%;

Score 418; DB 2;

Length 142;

Best Local Similarity

70.1%;

Score 418; DB 2;

Length 142;

Best Local Similarity

70.1%;

Score 418; DB 2;

Length 142;

Best Local Similarity

70.1%;

Score 418; DB 2;

Length 142;

Best Local Similarity

70.1%;

Score 418; DB 2;

Length 142;

Best Local Similarity

70.1%;

Score 418; DB 2;

Length 142;

Best Local Similarity

70.1%;

Score 418; DB 2;

Length 142;

ALIGNMENTS

RESULT 1
 A32483
 Ig heavy chain V region - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
 C;Accession: A32483
 R;Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abramson, M.; Fry, K.E.; Borrebaeck, C
 Biochem. Biophys. Res. Commun. 160, 1250-1255, 1989
 A;Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells usi
 A;Reference number: A32483; MUID:89273586; PMID:2499327
 A;Accession: A32483
 A;Status: Preliminary
 A;Molecule type: mRNA
 A;Residues: 1-142 <LRR>
 A;Cross-references: GB:M26463
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 F;25-108/Domain: immunoglobulin homology <IMM>
 Query Match Score 418; DB 2; Length 142;
 Best Local Similarity 65.5%; Pred. No. 6.5e-32; Mismatches 17; Indels 14; Gaps 2;
 Matches 81;
 Description
 1 VOLLEQSGAEVKGPGASVTLVAVSS 114
 2 S36265
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 7 S36265
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C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.9%; Score 398.5; DB 2; Length 118;

Best Local Similarity 66.1%; Pred. No. 3.5e-30; Mismatches 78; Conservative 14; Mismatches 21; Indels 5; Gaps 2;

Db 2 VOLV-QSGAEVKKPGASVKVSKASGYTFTGYMHMWVRQAPQGLEMWGWINPNSGGTNY 60

Qy 1 VOLLEQSGAEVKRPGASVTISCOASRQDFPSQYTHWVRQAPQGQFEMGGINPSSGSANY 60

Db 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 61 AOKFOGRVITRDTSASTAYMELSSLRS ETD TAVYV CARDFLSQYDLYWQGQMLTVSS 118

RESULT 3

S20783 Ig heavy chain V region - human

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

C;Accession: S20783

R;Morari, F.; Wang, J.; Schroeder, H.W.

Submitted to the EMBL Data Library, April 1992

A;Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.

A;Reference number: S20783

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-121 <KIP>

A;Cross-references: EMBL:211957; NID:93899; PID:CAA7014.1; PID:933900

C;Superfamily: Immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match Best Local Similarity 62.0%; Score 391; DB 2; Length 121; Matches 75; Conservative 16; Mismatches 22; Indels 8; Gaps 2;

Db 1 VOLLEQSGAEVKRPGASVTISCOASRQDFPSQYTHWVRQAPQGQFEMGGINPSSGSANY 60

Qy 2 VOLV-QSGAEVKKPGASVKVSKASGYTFTGYMHMWVRQAPQGLEMWGWINPNSGGTNY 60

Query Match 65.6%; Score 391; DB 2; Length 121; Matches 75; Conservative 16; Mismatches 22; Indels 8; Gaps 2;

Db 1 VOLLEQSGAEVKRPGASVTISCOASRQDFPSQYTHWVRQAPQGQFEMGGINPSSGSANY 60

Qy 2 VOLV-QSGAEVKKPGASVKVSKASGYTFTGYMHMWVRQAPQGLEMWGWINPNSGGTNY 60

Query Match Best Local Similarity 62.0%; Score 385; DB 2; Length 123; Matches 74; Conservative 17; Mismatches 22; Indels 10; Gaps 2;

Db 1 VOLLEQSGAEVKRPGASVTISCOASRQDFPSQYTHWVRQAPQGQFEMGGINPSSGSANY 60

Qy 2 VOLV-QSGAEVKKPGASVKVSKASGYTFTGYMHMWVRQAPQGLEMWGWINPNSGGTNY 60

Query Match Best Local Similarity 62.0%; Score 385; DB 2; Length 123; Matches 74; Conservative 17; Mismatches 22; Indels 10; Gaps 2;

Db 1 VOLLEQSGAEVKRPGASVTISCOASRQDFPSQYTHWVRQAPQGQFEMGGINPSSGSANY 60

Qy 2 VOLV-QSGAEVKKPGASVKVSKASGYTFTGYMHMWVRQAPQGLEMWGWINPNSGGTNY 60

Query Match Best Local Similarity 62.0%; Score 385; DB 2; Length 123; Matches 74; Conservative 17; Mismatches 22; Indels 10; Gaps 2;

Db 1 VOLLEQSGAEVKRPGASVTISCOASRQDFPSQYTHWVRQAPQGQFEMGGINPSSGSANY 60

Qy 2 VOLV-QSGAEVKKPGASVKVSKASGYTFTGYMHMWVRQAPQGLEMWGWINPNSGGTNY 60

Query Match Best Local Similarity 62.0%; Score 385; DB 2; Length 123; Matches 74; Conservative 17; Mismatches 22; Indels 10; Gaps 2;

Db 1 VOLLEQSGAEVKRPGASVTISCOASRQDFPSQYTHWVRQAPQGQFEMGGINPSSGSANY 60

Qy 2 VOLV-QSGAEVKKPGASVKVSKASGYTFTGYMHMWVRQAPQGLEMWGWINPNSGGTNY 60

Query Match Best Local Similarity 62.0%; Score 385; DB 2; Length 123; Matches 74; Conservative 17; Mismatches 22; Indels 10; Gaps 2;

Db 1 VOLLEQSGAEVKRPGASVTISCOASRQDFPSQYTHWVRQAPQGQFEMGGINPSSGSANY 60

Qy 2 VOLV-QSGAEVKKPGASVKVSKASGYTFTGYMHMWVRQAPQGLEMWGWINPNSGGTNY 60

Query Match Best Local Similarity 62.0%; Score 385; DB 2; Length 123; Matches 74; Conservative 17; Mismatches 22; Indels 10; Gaps 2;

Db 1 VOLLEQSGAEVKRPGASVTISCOASRQDFPSQYTHWVRQAPQGQFEMGGINPSSGSANY 60

Qy 2 VOLV-QSGAEVKKPGASVKVSKASGYTFTGYMHMWVRQAPQGLEMWGWINPNSGGTNY 60

Query Match Best Local Similarity 62.0%; Score 385; DB 2; Length 123; Matches 74; Conservative 17; Mismatches 22; Indels 10; Gaps 2;

Db 1 VOLLEQSGAEVKRPGASVTISCOASRQDFPSQYTHWVRQAPQGQFEMGGINPSSGSANY 60

Qy 2 VOLV-QSGAEVKKPGASVKVSKASGYTFTGYMHMWVRQAPQGLEMWGWINPNSGGTNY 60

Query Match Best Local Similarity 62.0%; Score 385; DB 2; Length 123; Matches 74; Conservative 17; Mismatches 22; Indels 10; Gaps 2;

Db 1 VOLLEQSGAEVKRPGASVTISCOASRQDFPSQYTHWVRQAPQGQFEMGGINPSSGSANY 60

Qy 2 VOLV-QSGAEVKKPGASVKVSKASGYTFTGYMHMWVRQAPQGLEMWGWINPNSGGTNY 60

RESULT 4

S49530 anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human

C;Species: Homo sapiens (man)

C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999

C;Accession: S49530

R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.

Submitted to the EMBL Data Library, October 1994

A;Description: Molecular characterization of natural human anti-Sm autoantibodies.

A;Reference number: S49530

A;Accession: S49530

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-135 <MAH>

A;Cross-references: EMBL:246348; NID:9560839; PID:CAA6467.1; PMID:9560840

C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match Best Local Similarity 65.2%; Score 388.5; DB 2; Length 135; Matches 75; Conservative 14; Mismatches 24; Indels 3; Gaps 2;

Qy 1 VOLLEQSGAEVKRPGASVTISCOASRQDFPSQYTHWVRQAPQGQFEMGGINPSSGSANY 60

Db 2 VOLV-QSGAEVKKPGASVKVSKASGYTFTGYMHMWVRQAPQGLEMWGWINPNSGGTNY 79

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Qy 61 APKFGRLLMSRDSSTDVMTSLTSED TAVYVC-LLKQAKHMGQGTIVAVSS 114

Db 80 AOKFOGRVITRDTISIATAYNELSRLRSDDTAVYV CARAR TYGNYWGQGTIVAVSS 135

Db	61	AQKFGGRVMTMDTTSVYMEISSLRSQEDTAVYVC
Db	62	PPKFRGRVMTMDTTSVYMEISSLRSQEDTAVYVC
Qy	112	VSS 114
Db	122	VSS 124
RESULT 7		
HRHNG		
Ig heavy chain precursor V-I region (HGS3) - human		
C;Species: Homo sapiens (man)		
C;Accession: A02024		
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004		
C;Rechavi, G.; Ram, D.; Glaser, L.; Zukut, R.; Givol, D.		
Proc. Natl. Acad. Sci. U.S.A. 80, 855-859, 1983		
A;Title: Evolutionary aspects of immunoglobulin heavy chain variable region (V-H) genes		
A;Reference number: A02024; NID:83144028; PMID:6298778		
A;Accession: A02024		
A;Molecule type: DNA		
A;Residues: 1-117 <REC>		
A;Cross-references: UNIPROT:D01743		
A;Note: the sequence was determined from the germline gene		
C;Genetic: GDB:IGHV@		
A;Cross-references: GDB:128528; OMIM:147070		
A;Map Position: 14q32.33-14q32.33		
A;Intron: 16/1		
C;Superfamily: immunoglobulin V region; immunoglobulin homology		
C;Keywords: heterotetramer; immunoglobulin		
F;1-19/Domain: signal sequence #status predicted <SIG>		
F;20-117/Product: Ig heavy chain V-I region (HGS)		
F;34-117/Domain: immunoglobulin homology <IMM>		
Query Match 63.2%; Score 376.5; DB 1; Length 117; Best Local Similarity 74.0%; Pred. No. 3.8e-28; Matches 71; Conservative 12; Mismatches 1; Indels 1; Gaps 1;		
Qy 1 VOLLEQSGAEVKRPGASVITISQASRQDFSGQYIHWVRQAPGQGEWMGGINPSGSANY 60		
Db 21 VOLV-QSGAEVKRPGASVITISQASRQDFSGQYIHWVRQAPGQGEWMGGINPSGSANY 79		
Qy 61 APKFKGRITMRSRDSSTDTVYMLTSLTSEDTAVYVC 96		
Db 80 AQKFGGRVMTMDTTSVYMEISSLRSQEDTAVYVC 115		
RESULT 8		
IG heavy chain V region (BO) - human (fragment)		
C;Species: Homo sapiens (man)		
C;Accession: I44151		
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 28-May-1999		
C;Accession: I44151		
R;Zebdeee, S.L.; Barbas III, C.F.; Hom, Y.L.; Cachhien, R.H.; Graff, R.; DeGraw, J.; Pyay, T.; Prok, Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992		
A;Title: Human combinatorial antibody libraries to hepatitis B surface antigen.		
A;Reference number: A44151; MUID:92228746; PMID:1373487		
A;Accession: I44151		
A;Status: preliminary; not compared with conceptual translation		
A;Molecule type: mRNA		
A;Residue: 1-125 <EB>		
A;Cross-references: GB:M88309; NID:9183952; PIDN:AAA35967.1; PID:9183953		
A;Note: nucleotide translation not given		
C;Superfamily: immunoglobulin V region; immunoglobulin homology		
C;Keywords: heterotetramer; immunoglobulin		
F;16-99/Domain: immunoglobulin homology <IMM>		
Query Match 62.8%; Score 374; DB 2; Length 126; Best Local Similarity 58.5%; Pred. No. 7e-28; Matches 72; Conservative 18; Mismatches 23; Indels 10; Gaps 2;		
Qy 1 VOLLEQSGAEVKRPGASVITISQASRQDFSGQYIHWVRQAPGQGEWMGGINPSGSANY 60		
Db 3 VKLJUE-SGAEVKRPQGAVKVKVSKCAGTYFPGYVWHRQAPGQGEWMGWIHPNGGTFH 61		
Qy 61 APKFKGRITMRSRDSSTDTVYMLTSLTSEDTAVYVC 111		
Db 121 KGTIVVSS 129		
RESULT 9		
HRHNG		
Ig heavy chain precursor V-I region (71-31) (anti-HIV-1) - human		
C;Species: Homo sapiens (man)		
C;Accession: C41287		
C;Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 21-Jan-2000		
C;Accession: C41287		
R;Andris, J.S.; Johnson, S.; Zolla-Pazner, S.; Capra, J.D.		
Proc. Natl. Acad. Sci. U.S.A. 88, 7783-7787, 1991		
A;Title: Molecular characterization of five human anti-human immunodeficiency virus		
A;Reference number: A41287; MUID:91352074; PMID:1909030		
A;Accession: C41287		
A;Status: preliminary		
A;Molecule type: mRNA		
A;Residues: 1-137 <AND>		
A;Cross-references: GB:M67502; NID:9185409; PIDN:AAA52943.1; PID:9185410		
C;Superfamily: immunoglobulin V region; immunoglobulin homology		
C;Keywords: heterotetramer; immunoglobulin		
F;34-116/Domain: immunoglobulin homology <IMM>		
Query Match 61.5%; Score 366.5; DB 2; length 137; Best Local Similarity 62.2%; Pred. No. 3.8e-27; Matches 74; Conservative 15; Mismatches 23; Indels 7; Gaps 3;		
Qy 1 VOLLEQSGAEVKRPGASVITISQASRQDFSGQYIHWVRQAPGQGEWMGGINPSGSANY 60		
Db 21 VOLV-QSGAEVKRPGASVITISQASRQDFSGQYIHWVRQAPGQGEWMGGINPSGSANY 78		
Qy 61 APKFKGRITMRSRDSSTDTVYMLTSLTSEDTAVYVC----LQALKHNGQTLIVAVSS 114		
Db 79 SOKFGQVAMRDTTSVAVIEMISSLRSVDMIYIYCAVQVAPLGLDQWGSLSVTSS 137		
Qy 546393		
Db 546393		
RESULT 10		
Ig heavy chain V region - human		
C;Species: Homo sapiens (man)		
C;Accession: S66333		
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.		
J. Mol. Biol. 239, 68-78, 1994		
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage		
A;Reference number: S66390; MUID:94254092; PMID:8196048		
A;Accession: S66393		
A;Status: preliminary		
A;Molecule type: DNA		
A;Residues: 1-129 <FIG>		
A;Cross-references: EMBL:Z31680; NID:9509786; PIDN:CAA83485.1; PID:91335146		
C;Keywords: heterotetramer; immunoglobulin		
F;15-98/Domain: immunoglobulin V region; immunoglobulin homology		
Query Match 61.2%; Score 365; DB 2; Length 129; Best Local Similarity 55.8%; Pred. No. 4.9e-27; Matches 72; Conservative 16; Mismatches 16; Indels 16; Gaps 2;		
Qy 1 VOLLEQSGAEVKRPGASVITISQASRQDFSGQYIHWVRQAPGQGEWMGGINPSGSANY 60		
Db 2 VOLV-QSGAEVKRPGASVITISQASRQDFSGQYIHWVRQAPGQGEWMGGINPSGSANY 60		
Qy 61 APKFKGRITMRSRDSSTDTVYMLTSLTSEDTAVYVC 105		
Db 61 AQKFGQVAMRDTTSVAVIEMISSLRSVDMIYIYCAVQVAPLGLDQWGSLSVTSS 120		
Qy 106 QGTIVVSS 114		
Db 121 KGTIVVSS 129		

RESULT 11

Ig heavy chain V region (clone 3B2) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

C:Accession: PH1669

R: Hillson, J. L.; Karr, N. S.; Oppiger, I. R.; Mannik, M.; Sasso, E. H.

J: Exp. Med. 178, 331-336, 1993

A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A. Reference number: PH1642; MUID:93301610; PMID:8315388

A:Accession: PH1669

A: Molecule type: mRNA

A: Residues: 1-110 <HIL>

A: Experimental source: B cell

C: Superfamily: immunoglobulin V region; immunoglobulin homology <IMM> F,7-90/Domain: immunoglobulin homology <IMM>

Query Match 60.7%; Score 362; DB 2; Length 110; Best Local Similarity 62.7%; Pred. No. 8e-27; Mismatches 25; Indels 4; Gaps 1; Matches 69; Conservative 12; Mismatches 25; Indels 4; Gaps 1; Matches 69; Conservative 17; Mismatches 27; Indels 13; Gaps 2; Db

QY 9 AEVRKGPGASVTTISQASROPSQGYIHWRRQAOQGFEWMMGINPSSGANY 60

1 AEVRKGPGASVKKVSKASGTYFTGMMWVRAOQGQLEWMGWINANSGCTYAQKFQGRV 60

Db

RESULT 12

Ig heavy chain V region (clone 3C5) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

C:Accession: PH1668

R: Hillson, J. L.; Karr, N. S.; Oppiger, I. R.; Mannik, M.; Sasso, E. H.

J: Exp. Med. 178, 331-336, 1993

A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A. Reference number: PH1642; MUID:93301610; PMID:8315388

A:Accession: PH1668

A: Molecule type: mRNA

A: Residues: 1-109 <HIL>

A: Experimental source: B cell

C:Keywords: heterotetramer; immunoglobulin homology <IMM>

F,7-90/Domain: immunoglobulin homology <IMM>

Query Match 60.7%; Score 362; DB 2; Length 110; Best Local Similarity 62.7%; Pred. No. 8e-27; Mismatches 25; Indels 4; Gaps 1; Matches 69; Conservative 12; Mismatches 25; Indels 4; Gaps 1; Matches 69; Conservative 17; Mismatches 27; Indels 13; Gaps 2; Db

QY 9 AEVRKGPGASVTTISQASROPSQGYIHWRRQAOQGFEWMMGINPSSGANY 60

1 AEVRKGPGASVKKVSKASGTYFTGMMWVRAOQGQLEWMGWINANSGCTYAQKFQGRV 60

Db

RESULT 13

Ig heavy chain V region precursor - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S23623

R: Olee, T.; Lu, E. W.; Huang, D. F.; Soto-Gil, R. W.; Defteros, M.; Kozin, F.; Carson, D. A.; J. Exp. Med. 175, 831-842, 1992

A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from

Query Match 60.2%; Score 358.5; DB 2; Length 111; Best Local Similarity 54.8%; Pred. No. 2.7e-26; Mismatches 27; Indels 13; Gaps 2; Matches 69; Conservative 17; Mismatches 27; Indels 13; Gaps 2; Db

QY 1 VOLLEQSGAEVERPGASVTTISQASROPSQGYIHWRRQAOQGFEWMMGINPSSGANY 60

2 VOLV-QSGAEVERKGPGASVKKVSKASGTYFTGMMWVRAOQGQLEWMGWINANSGCTYAQKFQGRV 60

Db

RESULT 14

Ig heavy chain V-1 region (NEI) - human

C:Species: Homo sapiens (man)

C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996

C:Accession: A33548

R: Kipps, T. J.; Tomhave, E.; Pratt, L. F.; Duffy, S.; Chen, P. P.; Carson, D. A.

Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989

A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expression

A:Reference number: A33548; MUID:83145575; PMID:2303826

A:Accession: A33548

A: Status: Preliminary; not compared with conceptual translation

A: Molecule type: mRNA

A: Residues: 1-129 <KIP>

R: Martin, T.; Duffy, S. F.; Carson, D. A.; Kipps, T. J.

J: Exp. Med. 175, 983-991, 1992

A:Title: Evidence for somatic selection of natural autoantibodies.

A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0956

A: Status: nucleic acid sequence not shown

A: Molecule type: DNA

A: Residues: 1-129 <MAR>

C:Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>

F,1-30/Region: framework 1

F,15-98/Region: immunoglobulin homology <IMM>

F,31-35/Region: complementarity-determining 1

F,36-50/Region: framework 2

F,51-67/Region: complementarity-determining 2

F,68-98/Region: framework 3

F,99-117/Region: complementarity-determining 3

Query Match 60.1%; Score 358; DB 2; Length 129; Best Local Similarity 58.1%; Pred. No. 2.2e-26; Mismatches 26; Indels 16; Gaps 2; Matches 75; Conservative 12; Mismatches 26; Indels 16; Gaps 2; Db

QY 1 VOLLEQSGAEVERPGASVTTISQASROPSQGYIHWRRQAOQGFEWMMGINPSSGANY 60

2 VOLV-QSGAEVERKGPGASVKKVSKASGTYFTGMMWVRAOQGQLEWMGWINANSGCTYAQKFQGRV 60

Db

RESULT 15

Ig heavy chain V region precursor - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S23623

R: Olee, T.; Lu, E. W.; Huang, D. F.; Soto-Gil, R. W.; Defteros, M.; Kozin, F.; Carson, D. A.; J. Exp. Med. 175, 831-842, 1992

A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from

Query Match 60.1%; Score 358; DB 2; Length 129; Best Local Similarity 58.1%; Pred. No. 2.2e-26; Mismatches 26; Indels 16; Gaps 2; Matches 75; Conservative 12; Mismatches 26; Indels 16; Gaps 2; Db

QY 1 APKFKGKLMRSDSSTDVYMLTSLSITEDTAVVYCL-----LOALKHWG 105

2 VOLV-QSGAEVERKGPGASVKKVSKASGTYFTGMMWVRAOQGQLEWMGWINANSGCTYAQKFQGRV 105

Db

QY 1 106 QSGTLYAVASS 114

Db

Db 121 QGTLVTVSS 129

RESULT 15

PH0962

Ig heavy chain v region (G6, T-L42) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996

C:Accession: PH0962

R:Martin, T.; Duffy, S.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A:Title: Evidence for somatic selection of natural autoantibodies.

A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0952

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-120 <MAR>

C:Superfamily: immunoglobulin v region; immunoglobulin homology

C:Keywords: heteroretramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-50/Region: framework 2

F:51-67/Region: complementarity-determining 2

F:68-98/Region: framework 3

F:99-108/Region: complementarity-determining 3

Query Match 59.8%; Score 356.5; DB 2; Length 120;

Best Local Similarity 61.7%; Pred. No. 2.8e-26; Gaps 2;

Matches 74; Conservative 13; Mismatches 26; Indels 7;

Oy 1 VOLLEOSGAVKREGASVTSQASRQDGCGOYIHWRQPGOGRFEMGAINPSGGSANT 60

Db 2 VOLVY-QSGAVERKPGESSVKVSKASGGTFSYALISWRQPGQGLEWMGGIIPFGTANY 60

Oy 61 APKPKGRJLMSRDSTDTVMTLTSLSLTSEDTAVYCLQAL---KNGQGILIVASS 114

Db 61 AOKFOGRVITTADESTSTAYMELSLRSEDTAVYVACRGSGVAGRPHFDYWGQGLVTVSS 120

Search completed: November 9, 2005, 05:59:53

Job time : 40 secs

This Page Blank (USPTO)

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OM protein - protein search, using bw model

Run on: November 9, 2005, 05:52:18 ; Search time 22 Seconds

Title: US-09-936-964A-36

Perfect score: 596

Sequence: 1 VQLEQSGEVKVRQASVTI.....YCLQNLKHWGQGIVAVSS 114

Scoring table: BLOSUM62

Gappen 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/pctdata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/pctdata/1/iaa/6A_COMB.pep:*

3: /cgn2_6/pctdata/1/iaa/6B_COMB.pep:*

4: /cgn2_6/pctdata/1/iaa/6C_COMB.pep:*

5: /cgn2_6/pctdata/1/iaa/PCTUS_Comb.pep:*

6: /cgn2_6/pctdata/1/iaa/backfiles1.pep:*

Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	396.5	66.5	120	3	US-09-025-769B-36
2	396.5	66.5	120	3	US-09-025-769B-36
3	396.5	66.5	120	4	US-09-490-070A-36
4	396.5	66.5	120	4	US-09-490-070B-59
5	396.5	66.5	120	4	US-09-490-070B-59
6	396.5	66.5	120	4	US-09-490-153-36
7	396.5	66.5	120	4	US-09-490-324-36
8	396.5	66.5	120	4	US-09-490-324-59
9	391	65.6	123	1	US-09-477-877B-94
10	391	65.6	123	2	US-08-472-281A-94
11	389	65.3	117	3	US-09-025-769B-22
12	389	65.3	117	4	US-09-490-070A-22
13	389	65.3	117	4	US-09-490-070B-22
14	389	65.3	117	4	US-09-490-153-22
15	389	65.3	117	4	US-09-490-324-22
16	380	63.8	470	4	US-09-859-053-28
17	376.5	63.2	97	5	PCT-US-96-0948-16
18	376.5	63.2	97	5	PCT-US-96-0948-16
19	376.5	63.2	117	3	US-08-545-809A-128
20	373	62.7	116	2	US-08-561-521-41
21	373.5	62.7	116	5	PCT-US-95-01219-1
22	373.5	62.7	135	1	US-08-137-117D-102
23	373.5	62.7	135	2	US-08-136-777-102
24	373	62.6	121	4	US-09-254-180C-7
25	373	62.6	140	1	US-07-946-421-28
26	369	61.9	119	4	US-08-954-94
27	368.5	61.8	97	5	PCT-US-95-10033-13

ALIGNMENTS

RESULT 1	US-09-025-769B-36
Sequence 36, Application US/09025769	Patent No. 6300064
GENERAL INFORMATION:	
APPLICANT: Knappik, Achim	APPLICANT: Pack, Peter
APPLICANT: Ge, Liming	APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas	APPLICANT: Tschopp, Stephan
APPLICANT: Protein/(Poly)peptide libraries	APPLICANT: Tschopp, Stephan
NUMBER OF SEQUENCES: 373	NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:	
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave	ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas	STREET: 1251 Avenue of the Americas
CITY: New York	CITY: New York
STATE: New York	STATE: New York
COUNTRY: USA	COUNTRY: USA
ZIP: 10021	ZIP: 10021
COMPUTER READABLE FORM:	
MEDIUM TYPE: Floppy disk	MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible	COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS	OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent System Release #1.0, Version #1.30 (BPO)	SOFTWARE: Patent System Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09/025,769B	APPLICATION NUMBER: US-09/025,769B
FILING DATE: 18-FEB-1998	FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0	APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995	FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.	NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794	REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5	REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000	TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090	TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 36:	INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids	LENGTH: 120 amino acids
TYPE: amino acid	TYPE: amino acid
STRANDEDNESS:	STRANDEDNESS:
TOPOLOGY: linear	TOPOLOGY: linear
MOLECULAR TYPE: protein	MOLECULAR TYPE: protein
US-09-025-769B-36	US-09-025-769B-36

Query Match Score 66.5% ; DB 3; Length 120;
Best Local Similarity 64.2%; Pred. No. 1 8e-33; Mismatches 22; Indels 7; Gaps 2;
Matches 77; Conservative

RESULT 3
US-09-490-070A-36
; Sequence 36, Application US/09490070A
; Patent No. 6696248

9-490-070A-36
Inventor 36, Application US/09490070A
Inventor No. 6696248

White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sanderson, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 59:

Query Match 66.5%; Score 396.5; DB 4; Length 120;
Best Local Similarity 64.2%; Pred. No. 1.8e-33;
Matches 77; Conservative 14; Mismatches 22; Indels 7; Gaps 2;

Qy 1 VOLLEQSGAEVKRGKPGASVTSQSCRSQDPSGQYIHWVROAPGQCFEWNGIINPGGGANY 60
2 VOLV-QSGAEVKPGKPGASVKSCKASGYFTSYMMHWVROAPGQGLEWMQWINPNSGGINY 60

Qy 61 APKKGRLIMSRDSSSTDTVYMTLTSLTSEDTAVYCL----LQALKHMGQGTIWAASS 114
61 AOKFQGRVMTRDTSISTAYMELSSLRSBDTAVYVYCARWGGDGFYAMDYWGQGTIWTVSS 120

RESULT 5
US-09-490-153-35

Sequence 36, Application US/09490153

Patent No. 670684

GENERAL INFORMATION:

APPLICANT: Knapik, Achim

Pack, Peter

Ilag, Vic

Ge, Liming

Plueckhun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5

FILING DATE: 24-Jan-2000
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5

FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5

INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 36:

US-09-490-153-36

Query Match 66.5%; Score 396.5; DB 4; Length 120;
Best Local Similarity 64.2%; Pred. No. 1.8e-33;
Matches 77; Conservative 14; Mismatches 22; Indels 7; Gaps 2;

Qy 1 VOLLEQSGAEVKRGKPGASVTSQSCRSQDPSGQYIHWVROAPGQCFEWNGIINPGGGANY 60
2 VOLV-QSGAEVKPGKPGASVKSCKASGYFTSYMMHWVROAPGQGLEWMQWINPNSGGINY 60

Qy 61 APKKGRLIMSRDSSSTDTVYMTLTSLTSEDTAVYCL----LQALKHMGQGTIWAASS 114
61 AOKFQGRVMTRDTSISTAYMELSSLRSBDTAVYVYCARWGGDGFYAMDYWGQGTIWTVSS 120

RESULT 6

US-09-490-153-59

Sequence 59, Application US/09490153

Patent No. 670684

GENERAL INFORMATION:

APPLICANT: Knapik, Achim

Pack, Peter

Ilag, Vic

Ge, Liming

Plueckhun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 59:

US-09-490-153-59

Query Match 66.5%; Score 396.5; DB 4; Length 120;

Best Local Similarity 64.2%; Pred. No. 1.8e-33; Length 120;

Matches 77; Conservative 14; Mismatches 22; Indels 7; Gaps 2;

Qy 1 VOLLEQSGAEEVKPGASVTISQASRDFSGQYIHWROAQPGQFEWNGINPSGGANY 60

Db 2 VOLV-QSGAEEVKPGASVKVSCKASGYTFISYMMHWVRQAPGQGLEMWGWINPNSGGTNY 60

Qy 61 APKFKGRLTMSRSSTDVWMLTSLTSEDITAVYVCL----LQALKHMGQGTAVVSS 114

Db 61 AOKFOGRVIMTRDTSISTAYMEBLSSRLSBDTAVYVYCARWGGDFYAMDYWGQGTLYVSS 120

RESULT 7

US-09-490-324-36

Sequence 36, Application US/09490324

PATENT NO. 6828422

GENERAL INFORMATION:

APPLICANT: Knapik, Achim

Packer, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09-490-324

FILING DATE: 24-Jan-2000

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,774

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 36:

US-09-490-324-36

Query Match 66.5%; Score 396.5; DB 4; Length 120;

Best Local Similarity 64.2%; Pred. No. 1.8e-33; Length 120;

Matches 77; Conservative 14; Mismatches 22; Indels 7; Gaps 2;

Qy 1 VOLLEQSGAEEVKPGASVTISQASRDFSGQYIHWROAQPGQFEWNGINPSGGANY 60

Db 2 VOLV-QSGAEEVKPGASVKVSCKASGYTFISYMMHWVRQAPGQGLEMWGWINPNSGGTNY 60

Qy 61 APKFKGRLTMSRSSTDVWMLTSLTSEDITAVYVCL----LQALKHMGQGTAVVSS 114

Db 61 AOKFOGRVIMTRDTSISTAYMEBLSSRLSBDTAVYVYCARWGGDFYAMDYWGQGTLYVSS 120

RESULT 8

US-09-490-324-59

Sequence 59, Application US/09490324

PATENT NO. 6828422

GENERAL INFORMATION:

APPLICANT: Knapik, Achim

Packer, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09-490-324

FILING DATE: 24-Jan-2000

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,774

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 59:

US-09-490-324-59

RESULT 9
US-08-477-87B-94
; Sequence 94, Application US/08477877B

PATENT NO. 5730979

GENERAL INFORMATION:

APPLICANT: Latinne, Dominique

TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activ

NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS:

APPLICANT: Bazin, Herv

ADDRESSEE: Carella, Byrne, Bain, Gilfillan,

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477, 87B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/407, 009

FILING DATE: 29-MAR-1995

APPLICATION NUMBER: 08/119, 032

FILING DATE: 09-SEP-1993

APPLICATION NUMBER: 08/027, 008

FILING DATE: 05-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Olstein, Elliot M.

REGISTRATION NUMBER: 24, 025

REFERENCE/DOCKET NUMBER: 61750-146

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 94:

SEQUENCE CHARACTERISTICS:

LENGTH: 123 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: polypeptide

FEATURE: NAME/KEY: Human Amu 5-3 heavy chain variable region.

US-08-477-87B-94

Query Match 65.6%; Score 391; DB 1; Length 123;

Best Local Similarity 61.0%; Pred. No. 7e-33; Mismatches 75; Conservative 16; Gaps 2;

Fig 33

Query Match 65.6%; Score 391; DB 2; Length 123;
Best Local Similarity 61.0%; Pred. No. 7e-33; Mismatches 75; Conservative 16; Gaps 2;

Matches 11; Score 391; DB 2; Length 123;

Query Match 65.6%; Score 391; DB 1; Length 123;
Best Local Similarity 61.0%; Pred. No. 7e-33; Mismatches 75; Conservative 16; Gaps 2;

Matches 11; Score 391; DB 1; Length 123;

Query Match 65.6%; Score 391; DB 2; Length 123;

Best Local Similarity 61.0%; Pred. No. 7e-33; Mismatches 75; Conservative 16; Gaps 2;

Matches 11; Score 391; DB 2; Length 123;

Query Match 65.6%; Score 391; DB 1; Length 123;

Best Local Similarity 61.0%; Pred. No. 7e-33; Mismatches 75; Conservative 16; Gaps 2;

Matches 11; Score 391; DB 1; Length 123;

Query Match 65.6%; Score 391; DB 2; Length 123;

Best Local Similarity 61.0%; Pred. No. 7e-33; Mismatches 75; Conservative 16; Gaps 2;

Matches 11; Score 391; DB 2; Length 123;

Query Match 65.6%; Score 391; DB 1; Length 123;

Best Local Similarity 61.0%; Pred. No. 7e-33; Mismatches 75; Conservative 16; Gaps 2;

Matches 11; Score 391; DB 1; Length 123;

Query Match 65.6%; Score 391; DB 2; Length 123;

Best Local Similarity 61.0%; Pred. No. 7e-33; Mismatches 75; Conservative 16; Gaps 2;

Matches 11; Score 391; DB 2; Length 123;

RESULT 11

US-08-477-87B-94

Sequence 94, Application US/08477877B

PATENT NO. 5730979

GENERAL INFORMATION:

APPLICANT: Bazin, Herv

APPLICANT: Latinne, Dominique

TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activ

NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS:

APPLICANT: Bazin, Herv

ADDRESSEE: Carella, Byrne, Bain, Gilfillan,

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477, 87B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/407, 009

FILING DATE: 29-MAR-1995

APPLICATION NUMBER: 08/119, 032

FILING DATE: 09-SEP-1993

APPLICATION NUMBER: 08/027, 008

FILING DATE: 05-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Olstein, Elliot M.

REGISTRATION NUMBER: 24, 025

REFERENCE/DOCKET NUMBER: 61750-146

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 94:

SEQUENCE CHARACTERISTICS:

LENGTH: 123 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: polypeptide

FEATURE: NAME/KEY: Human Amu 5-3 heavy chain variable region.

US-08-477-87B-94

Query Match 65.6%; Score 391; DB 1; Length 123;

Best Local Similarity 61.0%; Pred. No. 7e-33; Mismatches 75; Conservative 16; Gaps 2;

Matches 11; Score 391; DB 1; Length 123;

Query Match 65.6%; Score 391; DB 2; Length 123;

Best Local Similarity 61.0%; Pred. No. 7e-33; Mismatches 75; Conservative 16; Gaps 2;

Matches 11; Score 391; DB 2; Length 123;

Query Match 65.6%; Score 391; DB 1; Length 123;

Best Local Similarity 61.0%; Pred. No. 7e-33; Mismatches 75; Conservative 16; Gaps 2;

Matches 11; Score 391; DB 1; Length 123;

RESULT 10

US-08-477-87B-94

Sequence 94, Application US/08477877B

PATENT NO. 5730979

GENERAL INFORMATION:

APPLICANT: Bazin, Herv

APPLICANT: Latinne, Dominique

TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activ

NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS:

APPLICANT: Bazin, Herv

ADDRESSEE: Carella, Byrne, Bain, Gilfillan,

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477, 87B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/407, 009

FILING DATE: 29-MAR-1995

APPLICATION NUMBER: 08/119, 032

FILING DATE: 09-SEP-1993

APPLICATION NUMBER: 08/027, 008

FILING DATE: 05-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Olstein, Elliot M.

REGISTRATION NUMBER: 24, 025

REFERENCE/DOCKET NUMBER: 61750-146

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 94:

SEQUENCE CHARACTERISTICS:

LENGTH: 123 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: polypeptide

FEATURE: NAME/KEY: Human Amu 5-3 heavy chain variable region.

US-08-477-87B-94

Query Match 65.6%; Score 391; DB 1; Length 123;

Best Local Similarity 61.0%; Pred. No. 7e-33; Mismatches 75; Conservative 16; Gaps 2;

Matches 11; Score 391; DB 1; Length 123;

Query Match 65.6%; Score 391; DB 2; Length 123;

Best Local Similarity 61.0%; Pred. No. 7e-33; Mismatches 75; Conservative 16; Gaps 2;

Matches 11; Score 391; DB 2; Length 123;

Query Match 65.6%; Score 391; DB 1; Length 123;

Best Local Similarity 61.0%; Pred. No. 7e-33; Mismatches 75; Conservative 16; Gaps 2;

Matches 11; Score 391; DB 1; Length 123;

Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Latrine, Dominique

APPLICANT: Kaplan, Ruth

APPLICANT: Kieber-Emmons, Thomas

APPLICANT: Postema, Christina E.

APPLICANT: White-Scharf, Mary

TITLE OF INVENTION: LO-CO2a Antibody and Uses

TITLE OF INVENTION: Therefor for Inhibiting

TITLE OF INVENTION: T-Cell Activation and

TITLE OF INVENTION: Proliferation

NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carella, Byrne, Bain, Gilfillan,

ADDRESS: 6 Becker Farm Road

CITY: Roseland

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477, 989B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/407, 009

FILING DATE: 29-MAR-1995

APPLICATION NUMBER: 08/119, 032

FILING DATE: 09-SEP-1993

APPLICATION NUMBER: 08/027, 008

FILING DATE: 05-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Olstein, Elliot M.

REGISTRATION NUMBER: 24, 025

REFERENCE/DOCKET NUMBER: 61-50-147

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27, 794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9000

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-025-769B-22

Query Match 65.3%; Score 389; DB 3; Length 117;

Best Local Similarity 64.1%; Pred. No. 1.1e-32;

Matches 75; Conservative 15; Mismatches 23; Indels 4; Gaps 2;

NAME/KEY: Human Amu 5-3 heavy chain variable

NAME/KEY: region.

FEATURE: 08-477-989B-94

Query Match 65.6%; Score 391; DB 2; Length 123;

Best Local Similarity 64.0%; Pred. No. 7e-33;

Matches 75; Conservative 16; Mismatches 22; Indels 10; Gaps 2;

NAME/KEY: Human Amu 5-3 heavy chain variable

NAME/KEY: region.

FEATURE: 08-477-989B-94

Query Match 65.6%; Score 391; DB 2; Length 123;

Best Local Similarity 64.0%; Pred. No. 7e-33;

Matches 75; Conservative 16; Mismatches 22; Indels 10; Gaps 2;

NAME/KEY: Human Amu 5-3 heavy chain variable

NAME/KEY: region.

RESULT 13

US-09-490-070A-22

; Sequence 22, Application US/09490070A

; Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming

APPLICANT: Moroney, Simon

APPLICANT: Blaekthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1221 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025, 769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27, 794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9000

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-025-769B-22

Query Match 65.3%; Score 389; DB 3; Length 117;

Best Local Similarity 64.1%; Pred. No. 1.1e-32;

Matches 75; Conservative 15; Mismatches 23; Indels 4; Gaps 2;

NAME/KEY: Human Amu 5-3 heavy chain variable

NAME/KEY: region.

FEATURE: 08-477-989B-94

Query Match 65.6%; Score 391; DB 2; Length 123;

Best Local Similarity 64.0%; Pred. No. 7e-33;

Matches 75; Conservative 16; Mismatches 22; Indels 10; Gaps 2;

NAME/KEY: Human Amu 5-3 heavy chain variable

NAME/KEY: region.

RESULT 13

US-09-490-070A-22

; Sequence 22, Application US/09490070A

; Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming

APPLICANT: Moroney, Simon

APPLICANT: Blaekthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: Colin G. Sanderson, Esq. c/o Heller Ehrman

White & McAuliffe

1 VOLLEQSGASAEVKRPGASVITISQASRQDFSGQYIHWMRQAPGQFEMWGINPSCGSANY 60

2 VOLV-OSGAEVKRPKGASVTKVSKCAGSYFTGYNHWRQAPGQFEMWGINPNSGNTY 60

61 APKKRGKRLTMSRDSSTDVMTLTSLSITSDTAVVYCLQ---ALKHWGQTLVAVS 114

61 AQQFQGRVMTRDTISIAYMELSLRSDDTAVVYCLQARDGQGFYWGQTLVAVS 117

112 VSS 114

121 VSS 123

STREET: 1666 K Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A
 FILING DATE: 24-Jan-2000
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Colin G. Sandrock, Esq.
 REGISTRATION NUMBER: 31,298
 REFERENCE/DOCKET NUMBER: 37629-0005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 912-2000
 TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
 LENGTH: 117 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>

MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 22:
 US-09-490-070A-22

Query Match 65.3%; Score 399; DB 4; Length 117;
 Best Local Similarity 64.1%; Pred. No. 1.1e-32;
 Matches 75; Conservative 15; Mismatches 23; Indels 4; Gaps 2;

Qy 1 VOLLEQSGAEVKRGASVTVISQASRQPFGQYTHWVQAPGQCFEWGGINPSSGGANY 60
 Db 2 VOLV-QSGAVKRGASVTVISQASRQPFGQYTHWVQAPGQCFEWGGINPNSGNTVY 60

Qy 61 APKEKGRIJMSRSSTDVTMUTSLTBDTAVYCYLQ--ALKHMGQGTAVSS 114
 Db 61 APKEKGRIJMSRSSTDVTMUTSLTBDTAVYCYLQ--ALKHMGQGTAVSS 114

RESULT 14 US-09-490-153-22

Sequence 22, Application US/09490153
 Patent No. 670484

GENERAL INFORMATION:
 APPLICANT: Knapik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Blueckhun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324
 FILING DATE: 24-Jan-2000
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,769
 FILING DATE: 18-FEB-1998
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 1-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORPHO/5

STREET: 1666 K Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 ZIP: 20006

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,769B
 FILING DATE: 18-FEB-1998
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)596-9000
 TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
 LENGTH: 117 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>

MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 22:
 US-09-490-153-22

Query Match 65.3%; Score 399; DB 4; Length 117;
 Best Local Similarity 64.1%; Pred. No. 1.1e-32;
 Matches 75; Conservative 15; Mismatches 23; Indels 4; Gaps 2;

Qy 1 VOLLEQSGAEVKRGASVTVISQASRQPFGQYTHWVQAPGQCFEWGGINPSSGGANY 60
 Db 2 VOLV-QSGAVKRGASVTVISQASRQPFGQYTHWVQAPGQCFEWGGINPNSGNTVY 60

Qy 61 APKEKGRIJMSRSSTDVTMUTSLTBDTAVYCYLQ--ALKHMGQGTAVSS 114
 Db 61 APKEKGRIJMSRSSTDVTMUTSLTBDTAVYCYLQ--ALKHMGQGTAVSS 114

RESULT 15 US-09-90-324-22

Sequence 22, Application US/09490324
 Patent No. 6828422

GENERAL INFORMATION:
 APPLICANT: Knapik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Blueckhun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,324
 FILING DATE: 24-Jan-2000
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,769
 FILING DATE: 18-FEB-1998
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 1-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDIEDNESS: <Unknown>
TOPLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-490-324-22

Query	Match	Score	Length
QY	1 VOLLEQSGAEVKRPQGSVITISQASRQDFSGQYIHWVRQARPGQPEMWGIIINPSGGANY	389	117
Db	2 VOLV-QSGAEVTKPKGASVKSCKASGYFTSYMMHWVRQAPGQGLEMWGWIINPSGNTNY	641	60
QY	61 APKFKGKRLTMWRSDDSTTVMLTFLSLSEDATAVYCLIQ--ALKHNGQGTLUVAASS	114	114
Db	61 AQKFGGRVMTDRDTSIATYMEELSLRSDDTAVYCCARDGDDGFDFYngQGTLUVSS	117	117

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: November 9, 2005, 05:52:18 ; Search time 166 Seconds
(without alignments)

265.607 Million cell updates/sec

Title: US-09-936-964a-36
Perfect score: 596
Sequence: 1 VQLEQESGAEVKRPQGASVTI..... YCLLQALKHKGQGQTLVAVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : A_GenSeq_16Dec04:
1: genseqp1980s:
2: genseqp1990s:
3: genseqp2000s:
4: genseqp2001s:
5: genseqp2002s:
6: genseqp2003s:
7: genseqp2003b:
8: genseqp2004s:
9:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	RESULT
1	596	100.0	114	3 AAB18864	1 AAB18864
2	596	100.0	114	3 AAB18860	1 AAB18864 standard; protein; 114 AA.
3	596	100.0	114	3 AAB18876	1 XX
4	596	100.0	114	3 AAB18862	1 AC
5	596	100.0	114	3 AAB18866	1 XX
6	590	99.0	114	3 AAB18868	1 DT 08-FEB-2001 (first entry)
7	598	98.7	114	3 AAB18858	1 DE Amino acid sequence of anti-p53 antibody heavy chain clone 163.7.
8	578	97.0	114	3 AAB18874	1 XX
9	564	94.6	114	3 AAB18892	1 XX
10	536	89.9	114	3 AAB18880	1 DR p53; antibody; immune response; vaccine; gene therapy; cancer; rheumatoid arthritis; coronary heart disease.
11	536	89.9	114	3 AAB18878	1 OS Homo sapiens.
12	89.9	114	3 AAB18870	1 XX	
13	536	89.9	114	3 AAB18856	1 PN WO2005770-A1.
14	536	89.9	114	3 AAB18872	1 XX
15	421	70.6	3	AY15127	1 PR (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
16	419.5	70.4	124	8 ADN08043	1 PT Ward RL, Coomber DWJ;
17	418	70.1	142	6 ADA47344	1 PT WPI: 2000-638249/61.
18	418	70.1	142	8 ADP84549	1 DR N_PSDB; ARA96141.
19	418	70.1	142	8 ADQ87928	1 XX
20	418	70.1	249	8 ADR23326	1 PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide fragments, useful in treatment and diagnosis of cancer, rheumatoid arthritis and coronary heart disease.
21	414	69.5	255	5 ABP45145	1 PT
22	414	69.5	7	ADG95972	1 CC The present sequence represents the heavy chain of an antibody reactive against p53. The antibody is obtained from vertebrate host expressing an immune response against a naturally occurring disease. The antibodies are useful in pharmaceutical compositions, which additionally contain chelators, drugs, products, toxins and imaging markers e.g. radionuclotopes or gadolinium. The polypeptide components of the antibodies are useful in vaccines for inducing an immune response against a disease in a vertebrate, for treatment and/or prophylaxis of disease and for detection purposes. The nucleic acid sequences can be used to detect a disease as well as for gene therapy and recombinant production of the polypeptides. In particular, the following can be treated cancer, rheumatoid arthritis and coronary heart disease. Cancers include carcinogenic tumours, tumours
23	413.5	69.4	245	5 ADP45908	1 CC
24	412	69.4	7	ADG96735	1 CC
25	69.1	117	8	ADS92880	1 CC

Ads92892 Human Myo
Ads92878 Human Myo
Ads92890 Human Myo
Ads30439 Human GMB
Abp46080 Human BLy
Abp6907 Single ch
Abp45167 Human BLy
Abp95994 Single ch
Abp676525 HCV El an
Abp4279 Human BLy
Abp45288 Human BLy
Abp96106 Single ch
Abp96115 Single ch
Abp45448 Human BLy
Abp96275 Single ch
Abp45972 Human BLy
Abp96799 Single ch
Abp03971 Molline-ex
Abp46079 Human BLy
Abp96905 Single ch

CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer, head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer, CC gastric cancer, brain cancer, bladder cancer, prostate cancer and CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours, e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma

CC SQ Sequence 114 AA;

Query Match 100.0%; Score 596; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.1e-46; Indels 0; Gaps 0;
Matches 114; Conservative 0; Mismatches 0;

Qy 1 VOLLEQSGAEVKRGASVTISCOASRQDFSGQYIHWROAPGQGEFNGINPSSGANY 60
Db 1 VOLLEQSGAEVKRGASVTISCOASRQDFSGQYIHWROAPGQGEFNGINPSSGANY 60

Qy 61 APKFKGRLLTMSRDSSTDVYMLTSLSBEDTAVYCYCLQLQALKHKGQGTIVAVSS 114
Db 61 APKFKGRLLTMSRDSSTDVYMLTSLSBEDTAVYCYCLQLQALKHKGQGTIVAVSS 114

RESULT 2

ID AAB18860 standard; protein: 114 AA.

AC AAB18860;

XX DT 08-FEB-2001 (first entry)

XX DE Amino acid sequence of anti-p53 antibody heavy chain clone 163.5.

XX KW p53; antibody; immune response; vaccine; gene therapy; cancer; rheumatoid arthritis; coronary heart disease.

XX OS Homo sapiens.

XX PN WO200056770-A1.

XX PD 28-SEP-2000.

XX PR 15-MAR-2000; 2000WO-AU000189.

XX PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.

XX PI Ward RL, Coomber DMJ;

XX DR WPI: 2000-638249/61.

XX DR N-PSDB; AAA96137.

XX PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide fragments, useful in treatment and diagnosis of cancer, rheumatoid arthritis and coronary heart disease.

XX PS Claim 30; Page 135; 163pp; English.

XX The present sequence represents the heavy chain of an antibody reactive against p53. The antibody is obtained from a vertebrate host expressing an immune response against a naturally occurring disease. The antibodies are useful in pharmaceutical compositions, which additionally contain chelators, drugs, prodrugs, toxins and imaging markers e.g. radioisotopes or gadolinium. The polypeptide components of the antibodies are useful in vaccines, for inducing an immune response against a disease in a vertebrate, for treatment and/or prophylaxis of disease and for detection purposes. The nucleic acid sequences can be used to detect a disease as well as for gene therapy and recombinant production of the polypeptides. In particular, the following can be treated cancer, rheumatoid arthritis and coronary heart disease. Cancers include carcinogenic tumours, tumours of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer, head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer, CC gastric cancer, brain cancer, bladder cancer, prostate cancer and CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours, e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma

CC SQ Sequence 114 AA;

Query Match 100.0%; Score 596; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.1e-46; Indels 0; Gaps 0;
Matches 114; Conservative 0; Mismatches 0;

Qy 1 VOLLEQSGAEVKRGASVTISCOASRQDFSGQYIHWROAPGQGEFNGINPSSGANY 60
Db 1 VOLLEQSGAEVKRGASVTISCOASRQDFSGQYIHWROAPGQGEFNGINPSSGANY 60

Qy 61 APKFKGRLLTMSRDSSTDVYMLTSLSBEDTAVYCYCLQLQALKHKGQGTIVAVSS 114
Db 61 APKFKGRLLTMSRDSSTDVYMLTSLSBEDTAVYCYCLQLQALKHKGQGTIVAVSS 114

RESULT 3

ID AAB18876 standard; protein: 114 AA.

AC AAB18876;

XX DT 08-FEB-2001 (first entry)

XX DE Amino acid sequence of anti-p53 antibody heavy chain clone 163.20.

XX KW p53; antibody; immune response; vaccine; gene therapy; cancer; rheumatoid arthritis; coronary heart disease.

XX OS Homo sapiens.

XX PN WO200056770-A1.

XX PD 28-SEP-2000.

XX PR 15-MAR-2000; 2000WO-AU000189.

XX PR 19-MAR-1999; 99AU-00009321.

XX PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.

XX PI Ward RL, Coomber DMJ;

XX DR WPI; 2000-638249/61.

XX DR N-PSDB; AAA96153.

XX PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide fragments, useful in treatment and diagnosis of cancer, rheumatoid arthritis and coronary heart disease.

XX PS Claim 30; Page 151; 163pp; English.

XX The present sequence represents the heavy chain of an antibody reactive against p53. The antibody is obtained from a vertebrate host expressing an immune response against a naturally occurring disease. The antibodies are useful in pharmaceutical compositions, which additionally contain chelators, drugs, prodrugs, toxins and imaging markers e.g. radioisotopes or gadolinium. The polypeptide components of the antibodies are useful in vaccines, for inducing an immune response against a disease in a vertebrate, for treatment and/or prophylaxis of disease and for detection purposes. The nucleic acid sequences can be used to detect a disease as well as for gene therapy and recombinant production of the polypeptides. In particular, the following can be treated cancer, rheumatoid arthritis and coronary heart disease. Cancers include carcinogenic tumours, tumours of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer, head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer, CC gastric cancer, brain cancer, bladder cancer, prostate cancer and CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours, e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma

CC SQ Sequence 114 AA;

RESULT 9
AAB18882
ID AAB18882 standard; protein; 114 AA..

DE XX Amino acid sequence of anti-p53 antibody heavy chain clone 163.23.
 KW p53; antibody; immune response; vaccine; gene therapy; cancer;
 KW rheumatoid arthritis; coronary heart disease.
 XX OS Homo sapiens.
 XX WO20056770-A1.
 XX PN XX
 XX PD XX
 XX PR XX
 XX 15-MAR-2000; 20000W0-AU000189.
 XX PR XX
 XX 19-MAR-1999; 99AU-00009321.
 PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
 XX PI Ward RL, Coomber DWJ;
 XX DR XX
 XX N-PSDB; AAA96157.
 XX WPI; 2000-638249/61.
 XX
 PT Poly nucleotides encoding anti-p53 antibodies, polypeptides and peptides
 PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
 PT arthritis and coronary heart disease.
 XX
 PS Claim 30: Page 155; 163PP; English.
 XX
 CC The present sequence represents the heavy chain of an antibody reactive
 CC against p53. The antibody is obtained from a vertebrate host expressing
 CC an immune response against a naturally occurring disease. The antibody
 CC is useful in pharmaceutical compositions, which additionally contain
 CC chelators, drugs, prodrugs, toxins and imaging markers e.g. radioisotopes
 CC or gadolinium. The polypeptide components of the antibodies are useful
 CC vaccines, for inducing an immune response against a disease in a
 CC vertebrate, for treatment and/or prophylaxis of disease and for diagnostic
 CC purposes. The nucleic acid sequences can be used to detect a disease
 CC well as for gene therapy and recombinant production of the polypeptide.
 CC In particular, the following can be treated cancer, rheumatoid arthritis
 CC and coronary heart disease. Cancers include carcinogenic tumours, tumour
 CC of epithelial origin, e.g. colo-rectal cancer, breast cancer, lung cancer,
 CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
 CC gastric cancer, brain cancer, bladder cancer, prostate cancer, mesenchymal tumours
 CC and urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours
 XX e.g. sarcoma, and haemopoietic tumours, e.g. B cell lymphoma
 XX
 SQ Sequence 114 AA;

RESULT 11

Query Match 89.9%; Score 536; DB 3; Length 114;
 Best Local Similarity 88.6%; Pred. No. 3.4e-41; Gaps
 Matches 101; Conservative 8; Mis matches 5; Indels 0; Gaps

QV 1 VOLLEQSGAEEVKRIGASVUTISQASRQDRPSGQYIHWVRQAPGQFEMWGIIINPSGSANTY
 Db 1 VOLLEQSGAEEVKRIGASVUTISQASRQDRPSGQYIHWVRQAPGQFEMWGIIINPSGSANTY

Qy 61 APKKGKGLMSRSRSSTDTYVMTLTSLTSDDTAVYVCLQALKWKGQGTIVAVSS 114
 61 APKKGKGLMSRSRSSTDTYVMTLTSLTSDDTAVYVCLQALKWKGQGTIVAVSS 114
 Db 61 APSFGQRGLMSRDASTINTVYKLUSSLTSDDTAVYVCLQALKWKGQGTIVAVSS 114

ID AAB18878
 XX AAB18878 standard; protein; 114 AA.
 AC XX
 DT XX
 DE 08-FEB-2001 (first entry)
 XX
 DE Amino acid sequence of anti-p53 antibody heavy chain clone 163.22.
 KW p53; antibody; immune response; vaccine; gene therapy; cancer;
 KW

XX KW rheumatoid arthritis; coronary heart disease.
 XX OS
 XX PN
 XX WO20056770-A1.
 XX PD 28-SEP-2000.
 XX 15-MAR-2000; 2000WO-AU000189.
 XX PR 19-MAR-1999; 99AU-00009321.
 XX PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
 XX PI Ward RL, Coomber DWJ;
 XX DR WPI; 2000-638249161.
 XX DR N-FSDB; AAA96115.
 PT Poly nucleotides encoding anti-p53 antibodies, polypeptides and peptide
 PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
 PT arthritis and coronary heart disease.
 XX PS
 Claim 30; Page 153; 163pp; English.
 XX
 CC The present sequence represents the heavy chain of an antibody reactive
 CC against p53. The antibody is obtained from a vertebrate host expressing
 CC an immune response against a naturally occurring disease. The antibodies
 CC are useful in pharmaceutical compositions, which additionally contain
 CC chelators, drugs, prodrugs, toxins and imaging markers e.g. radioisotopes
 CC or gadolinium. The polypeptide components of the antibodies are useful in
 CC vaccines, for inducing an immune response against a disease in a
 CC vertebrate, for treatment and/or prophylaxis of disease and for detection
 CC purposes. The nucleic acid sequences can be used to detect a disease as
 CC well as for gene therapy and recombinant production of the polypeptides.
 CC In particular, the following can be treated cancer, rheumatoid arthritis
 CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
 CC of epithelial origin, e.g. colorectal cancer, breast cancer, lung cancer,
 CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
 CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
 CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
 CC e.g. sarcoma, and haemopoietic tumours, e.g. B cell lymphoma
 XX
 Sequence 114 AA;
 Query Match 89.9%; Score 536; DB 3; Length 114;
 Back Col Similarity 88.6%; Prod No 2 46-41.

PN	WO200056770-A1.
PP	15-MAR-2000; 2000WO-AU000189.
PD	28-SEP-2000.
PR	19-MAR-1999; 99AU-00009321.
XX	(SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
PA	Ward RL, Coomber DWJ;
XX	Ward RL, Coomber DWJ;
PR	(SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
XX	Ward RL, Coomber DWJ;
DR	N-PSDB; AAA96147.
XX	N-PSDB; AAA96147.
PT	Polyucleotides encoding anti-p53 antibodies, polypeptides and peptide fragments, useful in treatment and diagnosis of cancer, rheumatoid arthritis and coronary heart disease.
XX	Polyucleotides encoding anti-p53 antibodies, polypeptides and peptide fragments, useful in treatment and diagnosis of cancer, rheumatoid arthritis and coronary heart disease.
PS	Claim 30; Page 145; 163pp; English.
XX	The present sequence represents the heavy chain of an antibody reactive against p53. The antibody is obtained from a vertebrate host expressing an immune response against a naturally occurring disease. The antibodies are useful in pharmaceutical compositions, which additionally contain chelators, drugs, prodrugs, toxins and imaging markers e.g. radioisotopes or gadolinium. The polypeptide components of the antibodies are useful in vaccines, for inducing an immune response against a disease in a vertebrate, for treatment and/or prophylaxis of disease and for detection purposes. The nucleic acid sequences can be used to detect a disease as well as for gene therapy and recombinant production of the polypeptides. In particular, the following can be treated cancer, rheumatoid arthritis and coronary heart disease. Cancers include carcinogenic tumours, tumours of epithelial origin, e.g. colo-rectal cancer, breast cancer, lung cancer, head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer, gastric cancer, brain cancer, bladder cancer, prostate cancer and urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours, e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.
XX	Sequence 114 AA;
Query Match	89.9%; Score 536; DB 3; Length 114;
Best Local Similarity	88.6%; Pred. No. 3.4e-41;
Matches	101; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
QY	1 VOLLEQSGAETVKRPGASVTISQASRQDSFGQYIHWVRQAPGQFEGWMGIINPSGGSANY 60
Db	1 VOLLEQSGAETVKRPGASVTISQASRQDSFGQYIHWVRQAPGQFEGWMGIINPSGGSANY 60
QY	61 APKFGKRLTMSRDSSTDVTMVLTSITSLTSEDTAVYCLQALKHMGQGTIVAVSS 114
Db	61 APKFGKRLTMSRDSSTDVTMVLTSITSLTSEDTAVYCLQALKHMGQGTIVAVSS 114
QY	61 APSFQGRLMSRDASTNTVIMKLSSLTSEDATVYCLSQALKYMGQGTIVAVSS 114
Db	61 APSFQGRLMSRDASTNTVIMKLSSLTSEDATVYCLSQALKYMGQGTIVAVSS 114
RESULT 13	
ID	AAB18856 standard; protein; 114 AA.
XX	AAB18856;
AC	08-FEB-2001 (first entry)
XX	Amino acid sequence of anti-p53 antibody heavy chain clone 163.16.
DE	p53; antibody; immune response; vaccine; gene therapy; cancer;
KW	rheumatoid arthritis; coronary heart disease.
KW	Homo sapiens.
OS	
XX	W0200056770-A1.
PN	28-SEP-2000.
PP	15-MAR-2000; 2000WO-AU000189.
XX	W0200056770-A1.
PR	19-MAR-1999; 99AU-00009321.
XX	

ua-09-936-964a-36.rag

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ON protein - protein search, using sw model

Run on:

November 9, 2005, 05:52:17 ; Search time 165 Seconds

289.083 Million cell updates/sec

Title: US-09-936-964a-36

Perfect score: 596

Sequence: 1 VQLEQESGAEVKRPQGAVTI..... YCLLQLKHMQGQTLVAVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Score: 596

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	418	70.1	142	14 US-10-171-452A-2
2	418	70.1	142	15 US-10-353-708-2
3	418	70.1	142	16 US-10-731-984-36
4	418	69.5	255	10 US-09-880-748-1156
5	414	69.5	255	15 US-10-294-418-1156
6	413.5	69.4	245	10 US-09-880-748-1919
7	413.5	69.4	245	15 US-10-294-418-1919
8	412	69.1	117	16 US-10-688-925-16
9	412	69.1	117	16 US-10-688-925-28
10	412	69.1	249	16 US-10-688-925-14
11	412	69.1	249	16 US-10-688-925-26

ALIGNMENTS

Score	Length	DB ID	Sequence	Length	DB ID	Sequence
12	411.5	69.0	241	17	US-10-935-290-72	Sequence 72, Appl
13	410	68.8	248	10	US-09-880-748-2091	Sequence 2091, Ap
14	410	68.8	248	15	US-10-293-418-2091	Sequence 2091, Ap
15	409	68.6	248	15	US-10-293-418-1178	Sequence 1178, Ap
16	409	68.6	248	15	US-10-293-418-12290	Sequence 13, Appl
17	408.5	68.5	249	16	US-10-466-242-13	Sequence 1299, Ap
18	408.5	68.5	249	10	US-09-880-748-12290	Sequence 1299, Ap
19	408.5	68.5	249	10	US-09-880-748-12290	Sequence 1299, Ap
20	408.5	68.5	249	15	US-10-293-418-12290	Sequence 1299, Ap
21	408.5	68.5	249	15	US-10-293-418-12290	Sequence 1299, Ap
22	408.5	68.5	251	10	US-09-880-748-1459	Sequence 1459, Ap
23	408.5	68.5	251	15	US-10-293-418-1459	Sequence 1459, Ap
24	408.5	68.5	254	15	US-10-293-418-1983	Sequence 1983, Ap
25	406.5	68.5	254	10	US-09-880-748-1983	Sequence 1983, Ap
26	407	68.3	258	15	US-10-293-418-2090	Sequence 2090, Ap
27	407	68.3	258	15	US-10-293-418-2090	Sequence 2090, Ap
28	406	68.1	118	16	US-10-466-242-29	Sequence 29, Appl
29	403.5	67.7	243	15	US-09-880-748-1947	Sequence 1947, Ap
30	401	67.7	243	15	US-09-880-748-1947	Sequence 1947, Ap
31	403.5	67.7	254	10	US-09-880-748-1961	Sequence 1961, Ap
32	403.5	67.7	254	15	US-10-293-418-1961	Sequence 1961, Ap
33	402.5	67.5	114	15	US-10-293-418-1741	Sequence 141, Appl
34	402	67.4	253	10	US-09-880-748-1359	Sequence 1359, Ap
35	402	67.4	253	15	US-10-293-418-1359	Sequence 1359, Ap
36	401	67.3	253	20	US-09-880-748-1767	Sequence 5, Appl
37	399.5	67.0	245	18	US-10-943-197-5	Sequence 899, Ap
38	399	66.9	247	10	US-09-880-748-1899	Sequence 899, Ap
39	399	66.9	247	15	US-10-293-418-1899	Sequence 899, Ap
40	399	66.9	248	10	US-09-880-748-959	Sequence 959, Ap
41	399	66.9	248	15	US-10-293-418-959	Sequence 959, Ap
42	399	66.9	256	10	US-09-880-748-1967	Sequence 967, Ap
43	399	66.9	256	15	US-10-293-418-1967	Sequence 967, Ap
44	398.5	66.9	132	9	US-09-811-737-10	Sequence 10, Appl
45	398.5	66.9	260	9	US-09-811-737-16	Sequence 16, Appl

Score	Length	DB ID	Sequence	Length	DB ID	Sequence
12	411.5	69.0	241	17	US-10-935-290-72	Sequence 72, Appl
13	410	68.8	248	10	US-09-880-748-2091	Sequence 2091, Ap
14	410	68.8	248	15	US-10-293-418-2091	Sequence 2091, Ap
15	409	68.6	248	15	US-10-293-418-1178	Sequence 1178, Ap
16	409	68.6	248	15	US-10-293-418-12290	Sequence 13, Appl
17	408.5	68.5	249	16	US-10-466-242-13	Sequence 1299, Ap
18	408.5	68.5	249	10	US-09-880-748-12290	Sequence 1299, Ap
19	408.5	68.5	249	10	US-09-880-748-12290	Sequence 1299, Ap
20	408.5	68.5	249	15	US-10-293-418-12290	Sequence 1299, Ap
21	408.5	68.5	249	15	US-10-293-418-12290	Sequence 1299, Ap
22	408.5	68.5	251	10	US-09-880-748-1459	Sequence 1459, Ap
23	408.5	68.5	251	15	US-10-293-418-1459	Sequence 1459, Ap
24	408.5	68.5	254	15	US-10-293-418-1983	Sequence 1983, Ap
25	406.5	68.5	254	10	US-09-880-748-1983	Sequence 1983, Ap
26	407	68.3	258	15	US-10-293-418-2090	Sequence 2090, Ap
27	407	68.3	258	15	US-10-293-418-2090	Sequence 2090, Ap
28	406	68.1	118	16	US-10-466-242-29	Sequence 29, Appl
29	403.5	67.7	243	15	US-09-880-748-1947	Sequence 1947, Ap
30	401	67.7	243	15	US-09-880-748-1947	Sequence 1947, Ap
31	403.5	67.7	254	10	US-09-880-748-1961	Sequence 1961, Ap
32	403.5	67.7	254	15	US-10-293-418-1961	Sequence 1961, Ap
33	402.5	67.5	114	15	US-10-293-418-1741	Sequence 141, Appl
34	402	67.4	253	10	US-09-880-748-1359	Sequence 1359, Ap
35	402	67.4	253	15	US-10-293-418-1359	Sequence 1359, Ap
36	401	67.3	253	20	US-09-880-748-1767	Sequence 5, Appl
37	399.5	67.0	245	18	US-10-943-197-5	Sequence 899, Ap
38	399	66.9	247	10	US-09-880-748-1899	Sequence 899, Ap
39	399	66.9	247	15	US-10-293-418-1899	Sequence 899, Ap
40	399	66.9	248	10	US-09-880-748-959	Sequence 959, Ap
41	399	66.9	248	15	US-10-293-418-959	Sequence 959, Ap
42	399	66.9	256	10	US-09-880-748-1967	Sequence 967, Ap
43	399	66.9	256	15	US-10-293-418-1967	Sequence 967, Ap
44	398.5	66.9	132	9	US-09-811-737-10	Sequence 10, Appl
45	398.5	66.9	260	9	US-09-811-737-16	Sequence 16, Appl

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Score: 596

Sequence: 1 VQLEQESGAEVKRPQGAVTI..... YCLLQLKHMQGQTLVAVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

RESULT 2
S-10-333-708-2
Sequence 2, Application US10353708
Publication No. US20030219403A1
GENERAL INFORMATION:
APPLICANT: Frewin, Mark

; Publication No. US20040175381A1
; Sequence 36, Application US/10731984
; GENERAL INFORMATION:
; APPLICANT: WINDSOR-HINES, Dawn
; APPLICANT: RAO, Patricia
; APPLICANT: RINGER, Douglas J.
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES
; FILE REFERENCE: TUN-022
; CURRENT APPLICATION NUMBER: US/10/731,984
; CURRENT FILING DATE: 2003-12-09
; PRIORITY APPLICATION NUMBER: 60/431839
; PRIORITY FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 36
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Synthetic Oligonucleotide
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-731-984-36
Query Match 70.1%; Score 418; DE
Best Local Similarity 63.8%; Pred. NO. 2.7
Matches 81; Conservative 15; Mismatches 36

APPLICANT: Hale, Debra
APPLICANT: Rao, Patricia
APPLICANT: Kornaga, Tadeusz
APPLICANT: Ringle, Douglas
APPLICANT: Cobbold, Stephen
APPLICANT: Winsor-Hines, Dawn
TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen
FILE REFERENCE: 6954583-73
CURRENT APPLICATION NUMBER: US/10/353 708
CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: US10/171,452
PRIOR FILING DATE: 2002-06-13
PCTO APPLICATION NUMBER: PCT/US /2002 A71

PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: US60/373,470
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: US60/345,194
PRIOR FILING DATE: 2002-10-19
PRIOR APPLICATION NUMBER: GB0122724.8
PRIOR FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: GB0114517.6
PRIOR FILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 60
SEQ ID NO: 2
LENGTH: 142
TYPE: PRT
ORGANISM: Homo sapiens
S-10-353-708-2

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Query Match 70.1%; Score 418; DB 15; Length 142;
Best Local Similarity 63.8%; Pred. No. 2.7e-31;
Matches 81; Conservative 15; MisMatches 17; Indels 14; Gaps 2;
b
1 VOLLEQSGAEVKRPQASVTISQASRQDFSGQVTHWWVTOAPGQCFEWGMGINTPGGGANY 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||| 12
VQLV QSGAEVKPGASVVKUSCKASGIFTINYMHWRQAPGQLEWMGIIINFSGNSTVY 70
b
61 APKFKGRLTMSRDSSTTVMYMTLTSLSEDTAVYCY-----LLOALKHWSQG 107
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||| 71
AQKFQGKVIMRDTSTTVMYMLSLRSEDTAVYCAREKLATTIFGVLLITGMDYWGQG 130

```

131 TLVTVSS 137

RESULT 8
US-10-688-925-16
; Sequence 16, Application US/10688925
; Publication No. US20040142382A1
; GENERAL INFORMATION:
; APPLICANT: Veldman, Geertruida et al.
; TITLE OF INVENTION: NEUTRALIZING ANTIBODIES AGAINST GDF 8 AND USES THEREFOR
; FILE REFERENCE: 08702.0020-00000
; CURRENT APPLICATION NUMBER: US/10/688, 925
; CURRENT FILING DATE: 2003-10-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-688-925-16

Query Match 69.1%; Score 412; DB 16; Length 117;
Best Local Similarity 69.2%; Pred. No. 8e-31; Mismatches 20; Indels 4; Gaps 2;
Matches 81; Conservative 12; Mismatches 20; Indels 4; Gaps 2;

Qy 1 VOLLEQSGAEVKRGASVTISQASRQDFSGQYIHWVQAPQGQFEMINGINPGSSANY 60
Db 2 VOLV-QSGAEVKRGASVKVSCKASGYFTSYIHWVQAPQGQFEMINGINPGSSTSY 60

Qy 61 APKFKGSLTMSRSSTDYVMTLTSLSSTEDAVYVYCLQ--ALKHMGQGTIVAVSS 114
Db 61 AOKFQGSLTMSRSSTDYVMTLTSLSSTEDAVYVYCLQ--ALKHMGQGTIVAVSS 117

RESULT 9
US-10-688-925-28
; Sequence 28, Application US/10688925
; Publication No. US20040142382A1
; GENERAL INFORMATION:
; APPLICANT: Veldman, Geertruida et al.
; TITLE OF INVENTION: NEUTRALIZING ANTIBODIES AGAINST GDF 8 AND USES THEREFOR
; FILE REFERENCE: 08702.0020-00000
; CURRENT APPLICATION NUMBER: US/10/688, 925
; CURRENT FILING DATE: 2003-10-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-688-925-28

Query Match 69.1%; Score 412; DB 16; Length 249;
Best Local Similarity 69.2%; Pred. No. 1.7e-30; Mismatches 20; Indels 4; Gaps 2;
Matches 81; Conservative 12; Mismatches 20; Indels 4; Gaps 2;

Qy 1 VOLLEQSGAEVKRGASVTISQASRQDFSGQYIHWVQAPQGQFEMINGINPGSSANY 60
Db 2 VOLV-QSGAEVKRGASVKVSCKASGYFTSYIHWVQAPQGQFEMINGINPGSSTSY 60

Qy 61 APKFKGSLTMSRSSTDYVMTLTSLSSTEDAVYVYCLQ--ALKHMGQGTIVAVSS 114
Db 61 AOKFQGSLTMSRSSTDYVMTLTSLSSTEDAVYVYCLQ--ALKHMGQGTIVAVSS 117

RESULT 10
US-10-688-925-14
; Sequence 14, Application US/10688925
; Publication No. US20040142382A1
; GENERAL INFORMATION:
; APPLICANT: Veldman, Geertruida et al.
; TITLE OF INVENTION: NEUTRALIZING ANTIBODIES AGAINST GDF 8 AND USES THEREFOR
; FILE REFERENCE: 08702.0020-00000
; CURRENT APPLICATION NUMBER: US/10/688, 925
; CURRENT FILING DATE: 2003-10-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 14
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-688-925-14

Query Match 69.1%; Score 412; DB 16; Length 249;
Best Local Similarity 69.2%; Pred. No. 1.7e-30; Mismatches 20; Indels 4; Gaps 2;
Matches 81; Conservative 12; Mismatches 20; Indels 4; Gaps 2;

Qy 1 VOLLEQSGAEVKRGASVTISQASRQDFSGQYIHWVQAPQGQFEMINGINPGSSANY 60
Db 2 VOLV-QSGAEVKRGASVKVSCKASGYFTSYIHWVQAPQGQFEMINGINPGSSTSY 60

Qy 61 APKFKGSLTMSRSSTDYVMTLTSLSSTEDAVYVYCLQ--ALKHMGQGTIVAVSS 114
Db 61 AOKFQGSLTMSRSSTDYVMTLTSLSSTEDAVYVYCLQ--ALKHMGQGTIVAVSS 117

RESULT 11
US-10-688-925-26
; Sequence 26, Application US/10688925
; Publication No. US20040142382A1
; GENERAL INFORMATION:
; APPLICANT: Veldman, Geertruida et al.
; TITLE OF INVENTION: NEUTRALIZING ANTIBODIES AGAINST GDF 8 AND USES THEREFOR
; FILE REFERENCE: 08702.0020-00000
; CURRENT APPLICATION NUMBER: US/10/688, 925
; CURRENT FILING DATE: 2003-10-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-688-925-26

Query Match 69.1%; Score 412; DB 16; Length 249;
Best Local Similarity 69.2%; Pred. No. 1.7e-30; Mismatches 20; Indels 4; Gaps 2;
Matches 81; Conservative 12; Mismatches 20; Indels 4; Gaps 2;

Qy 1 VOLLEQSGAEVKRGASVTISQASRQDFSGQYIHWVQAPQGQFEMINGINPGSSANY 60
Db 2 VOLV-QSGAEVKRGASVKVSCKASGYFTSYIHWVQAPQGQFEMINGINPGSSTSY 60

Qy 61 APKFKGSLTMSRSSTDYVMTLTSLSSTEDAVYVYCLQ--ALKHMGQGTIVAVSS 114
Db 61 AOKFQGSLTMSRSSTDYVMTLTSLSSTEDAVYVYCLQ--ALKHMGQGTIVAVSS 117

RESULT 12
US-10-935-290-72
; Sequence 72, Application US/10935290
; Publication No. US20050069522A1
; GENERAL INFORMATION:
; APPLICANT: Baker et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to GMAD
; FILE REFERENCE: PCT84P1
; CURRENT APPLICATION NUMBER: US/10/935, 290
; CURRENT FILING DATE: 2004-09-08
; PRIORITY APPLICATION NUMBER: PCT/US03/09625

PRIOR FILING DATE: 2003-03-28

PRIOR APPLICATION NUMBER: 60/3368,813

PRIOR FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 234

SEQ ID NO 72

LENGTH: 241

TYPE: PRT

ORGANISM: Artificial sequence

OTHER INFORMATION: scFv protein GMBC646

Query Match 69.0%; Score 411.5; DB 17; Length 241;

Best Local Similarity 66.9%; Pred. No. 1.9e-30; Matches 79; Conservative 17; Mismatches 17; Indels 5; Gaps 2;

QY 1 VOLLEQSGAVKVRPGASVTISQASRQDPSQGYIHWVRQAPGQFEMNGIINNSGGSAN 60

Db 2 VOLV-OSGAEVKPKPSAVKVSCKASGYFTSYIHWVRQAPGQGLEWMGIIINPSGGTSY 60

QY 61 APKFKGRLTMSRSSTDTVMUTLTSISBTDAVYCYC---LLQALKHMGCGTLVAVS 114

Db 61 AOKFQGRVMTRDTSSTVYMEULSLSRSDTAYFCARERFLRMDVWGRGTMVVS 118

PRIOR APPLICATION NUMBER: 60/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: 60/880,748

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: 60/880,748

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: 60/880,748

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

RESULT 13

US-09-880-748-2091

Sequence 2991, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYs

CURRENT APPLICATION NUMBER: PF523

CURRENT FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: US/09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: 60/880,748

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: 60/880,748

PRIOR FILING DATE: 2000-06-15

RESULT 14

US-10-293-418-2091

Sequence 2991, Application US/10293418

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYs

CURRENT APPLICATION NUMBER: PF522P2

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: 60/880,748

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: 60/880,748

PRIOR FILING DATE: 2000-06-15

RESULT 15

US-09-880-748-1178

Sequence 1178, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYs

CURRENT APPLICATION NUMBER: PF523

CURRENT FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: 60/880,748

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: 60/880,748

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-16

RESULT 16

US-09-880-748-2091

Sequence 2991, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYs

CURRENT APPLICATION NUMBER: PF523P2

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: 60/880,748

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: 60/880,748

PRIOR FILING DATE: 2000-06-15

US-09-980-748-1178

Query Match 68.6%; Score 409; DB 10; Length 248;
Best Local Similarity 64.8%; Pred. No. 3.3e-30;
Matches 81; Conservative 14; Mismatches 18; Indels 12; Gaps 2;
QY 1 VOLLEOSGAEVKRGASVTCISQASRQDPSQGQIHWTRQAPGOCPEMGIINPSGGSANY 60
Db 2 VOLV-QSGAEVKKPGASVKSCKASGYFTSYMEHWVROAPSGGLENGINPSGGTSY 60
QY 61 APKEKGRLTWSRSSTDVYMTLTSLTBDTAVYCL-----LQALKHKGQTL 109
Db 61 AQKEQGRVYMTDTSSTVYMEPLLRSRDTAVYICAREHYDLTGYSLLGMDVWGRQL 120
QY 110 VAVSS 114
Db 121 VTVSS 125

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